

RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/732,680

Source: OIPE

Date Processed by STIC: 12/21/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/732,680

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☒ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ☐ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ☐ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/732,680

DATE: 12/21/2000
 TIME: 10:16:48

Input Set : A:\LeA34147.app
 Output Set: N:\CRF3\12212000\I732680.raw

Does Not Comply
 Corrected Diskette Needed

3 <110> APPLICANT: Bayer Aktiengesellschaft.
 5 <120> TITLE OF INVENTION: Nucleic acids coding for new acetylcholine receptor beta subunits of
 6 insects
 9 <130> FILE REFERENCE: Le A 34 147
 11 <140> CURRENT APPLICATION NUMBER: US/09/732,680
 12 <141> CURRENT FILING DATE: 2000-12-08
 14 <150> PRIOR APPLICATION NUMBER: DE 199 59 582.8
 15 <151> PRIOR FILING DATE: 1999-12-10
 17 <160> NUMBER OF SEQ ID NOS: 4
 19 <170> SOFTWARE: PatentIn Ver. 2.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 1539
 23 <212> TYPE: DNA
 24 <213> ORGANISM: Drosophila melanogaster
 26 <220> FEATURE:
 27 <221> NAME/KEY: CDS
 28 <222> LOCATION: (43)..(1365)
 30 <400> SEQUENCE: 1
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 32 Met Thr Thr Thr
 33 1
 35 ccc aag ata aag gca cca gtt tcc ggt cct gga ctg cca cta ctg ctg 102
 36 Pro Lys Ile Lys Ala Pro Val Ser Gly Pro Gly Leu Pro Leu Leu Leu
 37 5 10 15 20
 39 caa atg cta atg ggg atg ctt ctt atg ggg ctg act tcc gtg cca ggc 150
 40 Gln Met Leu Met Gly Met Leu Leu Met Gly Leu Thr Ser Val Pro Gly
 41 25 30 35
 43 gcc act gcc acc gcg gac ccc aag aac gcc aat gtc aag gcc ctg gat 198
 44 Ala Thr Ala Thr Ala Asp Pro Lys Asn Ala Asn Val Lys Ala Leu Asp
 45 40 45 50
 47 cgc ctc cac gcc ggc ctg ttc acg aac tac gac agc gat gtg cag ccg 246
 48 Arg Leu His Ala Gly Leu Phe Thr Asn Tyr Asp Ser Asp Val Gln Pro
 49 55 60 65
 51 gtg ttc caa gga acc ccc acg aac gtg tcc ctg gaa atg gtg gtc acc 294
 52 Val Phe Gln Gly Thr Pro Thr Asn Val Ser Leu Glu Met Val Val Thr
 53 70 75 80
 55 tac ata gac atc gac gag ttg aac ggc aag ctg acc acc cac tgc tgg 342
 56 Tyr Ile Asp Ile Asp Glu Leu Asn Gly Lys Leu Thr Thr His Cys Trp
 57 85 90 95 100
 59 ctg aat ctc cga tgg aga gac gag gag cgc gtg tgg caa ccg tca caa 390
 60 Leu Asn Leu Arg Trp Arg Asp Glu Glu Arg Val Trp Gln Pro Ser Gln
 61 105 110 115
 63 tat gac aac atc acg cag atc act ttg aag tcc agc gag gtc tgg acc 438
 64 Tyr Asp Asn Ile Thr Gln Ile Thr Leu Lys Ser Ser Glu Val Trp Thr
 65 120 125 130
 67 ccc caa atc aca ctc ttc aac ggc gac gaa ggt ggc ctg atg gcc gaa 486
 68 Pro Gln Ile Thr Leu Phe Asn Gly Asp Glu Gly Gly Leu Met Ala Glu

see
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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/732,680 DATE: 12/21/2000
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 Output Set: N:\CRF3\12212000\I732680.raw

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71 acc cag gtg acc ctc agc cac gat ggc cac ttc cgg tgg atg cct cca 534
72 Thr Gln Val Thr Leu Ser His Asp Gly His Phe Arg Trp Met Pro Pro
73          150          155          160
75 gcc gtg tac acg gcc tac tgc gaa ctc aac atg ctc aac tgg ccc cac 582
76 Ala Val Tyr Thr Ala Tyr Cys Glu Leu Asn Met Leu Asn Trp Pro His
77 165          170          175          180
79 gac aag cag agc tgc aag ttg aag atc ggc tcc tgg ggc ctg aag gtc 630
80 Asp Lys Gln Ser Cys Lys Leu Lys Ile Gly Ser Trp Gly Leu Lys Val
81          185          190          195
83 gtc ctg ccg gag aac ggc acg gcg aga gga gag tcc ctt gac cac gac 678
84 Val Leu Pro Glu Asn Gly Thr Ala Arg Gly Glu Ser Leu Asp His Asp
85          200          205          210
87 gac ctg gtt cag tca ccg gag tgg gaa atc gtg gac tcg cga gcc cac 726
88 Asp Leu Val Gln Ser Pro Glu Trp Glu Ile Val Asp Ser Arg Ala His
89          215          220          225
91 ttt gtc agt cag gac tac tac ggc tac atg gag tac act ctg acg gct 774
92 Phe Val Ser Gln Asp Tyr Thr Gly Tyr Met Glu Tyr Thr Leu Thr Ala
93          230          235          240
95 cag cgg cgc tcc tcc atg tac acg gcc gtc atc tac aca ccc qcg tcc 822
96 Gln Arg Arg Ser Ser Met Tyr Thr Ala Val Ile Tyr Thr Pro Ala Ser
97 245          250          255          260
99 tgc atc gtc atc ctg gcc ctc tca gcc ttc tgg ctg cct ccc cac atg 870
100 Cys Ile Val Ile Leu Ala Leu Ser Ala Phe Trp Leu Pro Pro His Met
101          265          270          275
103 ggc gcc gag aag atc atg atc aac gcc ctg ctc atc atc gtg atc gcc 918
104 Gly Gly Glu Lys Ile Met Ile Asn Gly Leu Leu Ile Ile Val Ile Ala
105          280          285          290
107 gcc ttc ctc atg tac ttc gcc cag ctc ctg cca gtg ctg tcc aac aat 966
108 Ala Phe Leu Met Tyr Phe Ala Gln Leu Leu Pro Val Leu Ser Asn Asn
109          295          300          305
111 act cca ctt gtg gta atc ttc tac agc acc agc ctg ctg tat ctg agc 1014
112 Thr Pro Leu Val Val Ile Phe Tyr Ser Thr Ser Leu Leu Tyr Leu Ser
113          310          315          320
115 gtc tcc acc atc gtc gag gtt cta gtt ctg tac ctg gcc aca gcc aag 1062
116 Val Ser Thr Ile Val Glu Val Leu Val Leu Tyr Leu Ala Thr Gly Lys
117 325          330          335          340
119 cac aag agg cgc ctg ccg gag gcg ctg aga aag ctg ctg cac ggg cac 1110
120 His Lys Arg Arg Leu Pro Glu Ala Leu Arg Lys Leu Leu His Gly His
121          345          350          355
123 ctg gcc acg tgg ctg ctg ctc tcc gtg ttc agc acc act ggc gag tcc 1158
124 Leu Gly Thr Trp Leu Leu Leu Ser Val Phe Ser Thr Thr Gly Glu Ser
125          360          365          370
127 cag gcg gag aag acc aaa gag atg gac gag cac ccg tac gag gag gcg 1206
128 Gln Ala Glu Lys Thr Lys Glu Met Asp Glu His Pro Tyr Glu Glu Ala
129          375          380          385
131 gac gag cag gag tcc agt ccg ctg gcc atc aac cac acc gag gtg ccg 1254
132 Asp Glu Gln Glu Ser Ser Pro Leu Gly Ile Asn His Thr Glu Val Pro
133          390          395          400

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Input Set : A:\LeA34147.app
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136 Gly Ala Lys Ala Asn Gln Phe Asp Trp Ala Leu Leu Ala Thr Ala Val
137 405 410 415 420
139 gac cgc att tcc ttc gtt tcc ttc agc ctg gcc ttc ctc att ctg gcc 1350
140 Asp Arg Ile Ser Phe Val Ser Phe Ser Leu Ala Phe Leu Ile Leu Ala
141 425 430 435
143 atc aag tgc tcc gtg tagggatgct cgagacLcaa ggcacatcc caagccagtg 1405
144 Ile Arg Cys Ser Val
145 440
147 cgcactctga actagttttg catttgcgat ttcattgtatt taatgtgtgtl gcgaacttat 1465
149 aattattttaa tgatgagacc tegtatyga taaaggacct ctgccgaary tctgcttaca 1525
151 aaaaaaaaaa aaaa 1539
154 <210> SEQ ID NO: 2
155 <211> LENGTH: 441
156 <212> TYPE: PRT
157 <213> ORGANTSM: Drosophila melanogaster
159 <400> SEQUENCE: 2
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161 1 5 10 15
163 Pro Leu Leu Leu Gln Met Leu Met Gly Met Leu Leu Met Gly Leu Thr
164 20 25 30
166 Ser Val Pro Gly Ala Thr Ala Thr Ala Asp Pro Lys Asn Ala Asn Val
167 35 40 45
169 Lys Ala Leu Asp Arg Leu His Ala Gly Leu Phe Thr Asn Tyr Asp Ser
170 50 55 60
172 Asp Val Gln Pro Val Phe Gln Gly Thr Pro Thr Asn Val Ser Leu Glu
173 65 70 75 80
175 Met Val Val Thr Tyr Ile Asp Ile Asp Glu Leu Asn Gly Lys Leu Thr
176 85 90 95
178 Thr His Cys Trp Leu Asn Leu Arg Trp Arg Asp Glu Glu Arg Val Trp
179 100 105 110
181 Gln Pro Ser Gln Tyr Asp Asn Ile Thr Gln Ile Thr Leu Lys Ser Ser
182 115 120 125
184 Glu Val Trp Thr Pro Gln Ile Thr Leu Phe Asn Gly Asp Glu Gly Gly
185 130 135 140
187 Leu Met Ala Glu Thr Gln Val Thr Leu Ser His Asp Gly His Phe Arg
188 145 150 155 160
190 Trp Met Pro Pro Ala Val Tyr Thr Ala Tyr Cys Glu Leu Asn Met Leu
191 165 170 175
193 Asn Trp Pro His Asp Lys Gln Ser Cys Lys Leu Lys Ile Gly Ser Trp
194 180 185 190
196 Gly Leu Lys Val Val Leu Pro Glu Asn Gly Thr Ala Arg Gly Glu Ser
197 195 200 205
199 Leu Asp His Asp Asp Leu Val Gln Ser Pro Glu Trp Glu Ile Val Asp
200 210 215 220
202 Ser Arg Ala His Phe Val Ser Gln Asp Tyr Tyr Gly Tyr Met Glu Tyr
203 225 230 235 240
205 Thr Leu Thr Ala Gln Arg Arg Ser Ser Met Tyr Thr Ala Val Ile Tyr
206 245 250 255

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208 Thr Pro Ala Ser Cys Ile Val Ile Leu Ala Leu Ser Ala Phe Trp Leu
 209 260 265 270
 211 Pro Pro His Met Gly Gly Glu Lys Ile Met Ile Asn Gly Leu Leu Ile
 212 275 280 285
 214 Ile Val Ile Ala Ala Phe Leu Met Tyr Phe Ala Gln Leu Leu Pro Val
 215 290 295 300
 217 Leu Ser Asn Asn Thr Pro Leu Val Val Ile Phe Tyr Ser Thr Ser Leu
 218 305 310 315 320
 220 Leu Tyr Leu Ser Val Ser Thr Ile Val Glu Val Leu Val Leu Tyr Leu
 221 325 330 335
 223 Ala Thr Gly Lys His Lys Arg Arg Leu Pro Glu Ala Leu Arg Lys Leu
 224 340 345 350
 226 Leu His Gly His Leu Gly Thr Trp Leu Leu Leu Ser Val Phe Ser Thr
 227 355 360 365
 229 Thr Gly Glu Ser Gln Ala Glu Lys Thr Lys Glu Met Asp Glu His Pro
 230 370 375 380
 232 Tyr Glu Glu Ala Asp Glu Gln Glu Ser Ser Pro Leu Gly Ile Asn His
 233 385 390 395 400
 235 Thr Glu Val Pro Gly Ala Lys Ala Asn Gln Phe Asp Trp Ala Leu Leu
 236 405 410 415
 238 Ala Thr Ala Val Asp Arg Ile Ser Phe Val Ser Phe Ser Leu Ala Phe
 239 420 425 430
 241 Leu Ile Leu Ala Ile Arg Cys Ser Val
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246 <210> SEQ ID NO: 3

247 <211> LENGTH: 20

248 <212> TYPE: DNA

249 <213> ORGANISM: Artificial Sequence

251 <220> FEATURE:

252 <223> OTHER INFORMATION: Primer

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258 <210> SEQ ID NO: 4

259 <211> LENGTH: 21

260 <212> TYPE: DNA

261 <213> ORGANISM: Artificial Sequence

263 <220> FEATURE:

264 <223> OTHER INFORMATION: Primer

266 <400> SEQUENCE: 4

W--> 267 catratytty tcnccccc t

21

VERIFICATION SUMMARY

DATE: 12/21/2000

PATENT APPLICATION: US/09/732,680

TIME: 10:16:49

Input Set : A:\LeA34147.app

Output Set: N:\CRF3\12212000\I732680.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:255 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
L:255 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
L:255 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:3
L:267 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:267 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:267 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4